



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 149432

TO: Nita M Minnifield
Location: rem/3c01/3c18
Art Unit: 1645
Friday, April 01, 2005

Case Serial Number: 09/914454

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Minnifield,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



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Gen nucleic - nucleic search, using SW model

Run on: March 31, 2005, 17:42:45 ; Search time 125 Seconds
(without alignments)
395.473 Million cell updates/sec

Title: US-09-914-454b-1

Perfect score: 20

Sequence: 1 tccatgacgttcctgacgtt 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: EST*

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2: gb_est2:*
3: gb_hcc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	20	100.0	498	9	CL978668
2	20	100.0	2799	9	CL978665
3	18.4	92.0	886	9	CC709713
4	17.4	87.0	638	7	CN928980
5	17.4	87.0	1062	9	CL970339
6	17.4	85.0	1088	6	CD505499
7	17.4	85.0	2805	9	CL965273
8	16.8	84.0	287	2	BF713668
9	16.8	84.0	389	9	CG260054
10	16.8	84.0	464	1	AA117941
11	16.8	84.0	497	9	CL119555
12	16.8	84.0	516	2	BF156008
13	16.8	84.0	546	2	AM065908
14	16.8	84.0	557	6	CA158051
15	16.8	84.0	614	6	CA113844
16	16.8	84.0	646	6	CA109803
17	16.8	84.0	663	6	CA153904
18	16.8	84.0	668	6	CA264770
19	16.8	84.0	683	6	CA182313
20	16.8	84.0	715	5	BU253412
21	16.8	84.0	729	7	CV181077
22	16.8	84.0	758	8	CC110844
23	16.8	84.0	794	9	CG334934
24	16.8	84.0	797	9	CNS02N06

C	25	16.8	84.0	814	5	BU205165
C	26	16.8	84.0	821	9	CNS03084
C	27	16.8	84.0	842	9	CG319646
C	28	16.8	84.0	864	9	CG318330
C	29	16.8	84.0	908	6	CD791886
C	30	16.8	84.0	915	5	CG318342
C	31	16.8	84.0	958	5	BO882047
C	32	16.8	84.0	992	9	CNS04004
C	33	16.8	84.0	994	9	CNS0421L
C	34	16.8	84.0	1867	3	CR696760
C	35	16.4	82.0	179	4	BM598254
C	36	16.4	82.0	318	8	AZ578302
C	37	16.4	82.0	392	6	BY630307
C	38	16.4	82.0	398	4	BI033356
C	39	16.4	82.0	553	2	BB767360
C	40	16.4	82.0	596	4	BM592203
C	41	16.4	82.0	643	2	BE647310
C	42	16.4	82.0	648	2	BS529260
C	43	16.4	82.0	665	2	BB183341
C	44	16.4	82.0	680	1	AL694689
C	45	16.4	82.0	695	7	CF531954

ALIGNMENTS

RESULT 1
LOCUS CL978668
DEFINITION OeIFCC032298 Oryza sativa Expressed Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
ACCESSION CL978668
VERSION CL978668.1 GI:52411839
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Euphorbiaceae; Oryzae; Oryza.

REFERENCE

AUTHORS

JOURNAL

COMMENT

Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G. K. S., Deng, X. W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatics
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.

FEATURES

source
1..498
Location/Qualifiers
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Expressed Library"
/note="Oryza sativa exon trapped genomic sequences"

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 498;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ory 1 TCCATGACGTTCTGACGTT 20
DB 83 TCCATGACGTTCTGACGTT 64

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Gen Nucleic - nucleic search, using sw model

March 31, 2005, 17:00:28 ; Search time 312 Seconds
(without alignments)
387.980 Million cell updates/sec

File: US-09-914-454B-1

Perfect score: 20

Sequence: 1 tccatgacgttcctgacgtt 20

Scoring table: IDENTITY NTC

Gapop 10.0, Gapext 1.0

Searched: 5607317 seqs, 302624599 residues 11214634

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	20	100.0	20	9	US-09-824-468-100
4	20	100.0	20	9	US-09-824-468-105
5	20	100.0	20	9	US-09-949-194-1
6	20	100.0	20	9	US-09-917-222-1
7	20	100.0	20	9	US-09-800-266A-86
8	20	100.0	20	9	US-09-800-266A-90
9	20	100.0	20	9	US-09-895-007A-86
10	20	100.0	20	9	US-09-895-007A-90
11	20	100.0	20	9	US-09-920-313-86

12	20	100.0	20	9	US-09-920-313-90	Sequence 90, Appl
13	20	100.0	20	10	US-09-888-326-560	Sequence 560, App
14	20	100.0	20	10	US-09-888-326-561	Sequence 561, App
15	20	100.0	20	10	US-09-888-326-562	Sequence 562, App
16	20	100.0	20	10	US-09-888-326-563	Sequence 563, App
17	20	100.0	20	10	US-09-818-918-10	Sequence 10, Appl
18	20	100.0	20	10	US-09-931-583-47	Sequence 47, Appl
19	20	100.0	20	10	US-09-776-479-69	Sequence 69, Appl
20	20	100.0	20	10	US-09-776-479-137	Sequence 137, App
21	20	100.0	20	10	US-09-776-479-152	Sequence 152, App
22	20	100.0	20	10	US-09-776-479-223	Sequence 223, App
23	20	100.0	20	10	US-09-776-479-302	Sequence 302, App
24	20	100.0	20	10	US-09-776-479-948	Sequence 948, App
25	20	100.0	20	10	US-09-776-479-949	Sequence 949, App
26	20	100.0	20	10	US-09-776-479-950	Sequence 950, App
27	20	100.0	20	10	US-09-776-479-951	Sequence 951, App
28	20	100.0	20	10	US-09-776-479-952	Sequence 952, App
29	20	100.0	20	10	US-09-776-479-953	Sequence 953, App
30	20	100.0	20	10	US-09-776-479-954	Sequence 954, App
31	20	100.0	20	10	US-09-776-479-955	Sequence 955, App
32	20	100.0	20	10	US-09-776-479-956	Sequence 956, App
33	20	100.0	20	10	US-09-776-479-957	Sequence 957, App
34	20	100.0	20	10	US-09-776-479-958	Sequence 958, App
35	20	100.0	20	10	US-09-776-479-959	Sequence 959, App
36	20	100.0	20	10	US-09-776-479-960	Sequence 960, App
37	20	100.0	20	10	US-09-776-479-961	Sequence 961, App
38	20	100.0	20	10	US-09-776-479-962	Sequence 962, App
39	20	100.0	20	10	US-09-776-479-963	Sequence 963, App
40	20	100.0	20	10	US-09-776-479-964	Sequence 964, App
41	20	100.0	20	10	US-09-776-479-965	Sequence 965, App
42	20	100.0	20	10	US-09-776-479-966	Sequence 966, App
43	20	100.0	20	10	US-09-776-479-967	Sequence 967, App
44	20	100.0	20	10	US-09-776-479-968	Sequence 968, App
45	20	100.0	20	10	US-09-776-479-969	Sequence 969, App

ALIGNMENTS

RESULT 1

US-09-760-506-3

Sequence 3, Application US/09760506

Publication No. US20010034330A1

GENERAL INFORMATION:

APPLICANT: Kemsil, Charlotte

TITLE OF INVENTION: Innate Immunity-Stimulating Compositions of Cpg and

FILE REFERENCE: 8449-153-999

CURRENT APPLICATION NUMBER: US/09760, 506

PRIOR FILING DATE: 2002-01-12

PRIOR APPLICATION NUMBER: 60/200, 853

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: 60/175, 840

PRIOR FILING DATE: 2000-01-13

PRIOR APPLICATION NUMBER: 60/128, 608

PRIOR FILING DATE: 1999-04-08

PRIOR APPLICATION NUMBER: 60/095, 913

PRIOR FILING DATE: 1998-08-10

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn version 3.0

SEQ ID NO 3

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Motif

US-09-760-506-3

Query Match 100.0%; Score 20; DB 9; Length 20;

Best Local Similarity 100.0%; Pred. No. 4.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 tccatgacgttcctgacgtt 20

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Clustalw - nucleic search, using SW model

Run on:

March 31, 2005, 16:07:48 ; Search time 95 Seconds
(without alignments)
344.479 Million cell updates/sec

Title: US-09-914-454B-1

Perfect score: 20

Sequence: 1 tccatgacgttcttgacgtt 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 6: /cgn2_6/prodata/1/ina/5B_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	20	100.0	20	US-09-303-862-12	Sequence 12, Appl
3	20	100.0	20	US-08-738-652-10	Sequence 10, Appl
4	20	100.0	20	US-09-030-701-62	Sequence 10, Appl
5	20	100.0	20	US-09-286-098-100	Sequence 100, App
6	20	100.0	20	US-09-286-098-105	Sequence 105, App
7	20	100.0	20	US-08-960-774-10	Sequence 10, App
8	20	100.0	20	US-09-082-649B-51	Sequence 51, Appl
9	20	100.0	20	US-09-082-649B-56	Sequence 56, Appl
10	20	100.0	20	US-09-082-649B-58	Sequence 58, Appl
11	20	100.0	20	US-09-325-193A-86	Sequence 86, Appl
12	20	100.0	20	US-09-325-193A-90	Sequence 90, Appl
13	20	100.0	20	US-09-191-170-97	Sequence 97, Appl
14	20	100.0	20	US-09-690-921-1	Sequence 1, Appl
15	20	100.0	20	US-09-301-823A-1	Sequence 1, Appl
16	20	100.0	20	US-09-692-170C-42	Sequence 42, Appl
17	20	100.0	20	US-09-337-619-10	Sequence 42, Appl
18	20	100.0	20	US-10-405-231A-42	Sequence 42, Appl
19	20	100.0	20	US-10-238-607-42	Sequence 42, Appl
20	20	100.0	20	US-09-984-365-42	Sequence 42, Appl
21	20	100.0	20	US-09-565-906-1	Sequence 1, Appl
22	20	100.0	20	US-09-257-188A-2	Sequence 2, Appl
23	20	100.0	20	US-09-965-101-51	Sequence 51, Appl
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25	20	100.0	20	US-09-965-101-58	Sequence 58, Appl
26	20	100.0	20	US-09-082-649B-12	Sequence 12, Appl
27	20	100.0	20	US-09-082-649B-13	Sequence 13, Appl

28	20	100.0	44	US-09-965-101-12	Sequence 12, Appl
29	20	100.0	44	US-09-965-101-13	Sequence 13, Appl
30	17	85.0	17	US-09-030-701-39	Sequence 19, Appl
31	17	85.0	17	US-09-286-098-70	Sequence 70, Appl
32	17	85.0	17	US-08-960-774-70	Sequence 70, Appl
33	17	85.0	17	US-09-325-193A-60	Sequence 60, Appl
34	17	85.0	17	US-09-191-170-64	Sequence 64, Appl
35	17	85.0	17	US-09-337-619-70	Sequence 70, Appl
36	16.8	84.0	20	US-09-133-774-11	Sequence 11, Appl
37	16.8	84.0	20	US-08-386-063-25	Sequence 25, Appl
38	16.8	84.0	20	US-09-303-862-11	Sequence 11, Appl
39	16.8	84.0	20	US-08-386-063-25	Sequence 25, Appl
40	16.8	84.0	20	US-08-738-652-35	Sequence 35, Appl
41	16.8	84.0	20	US-08-738-652-44	Sequence 44, Appl
42	16.8	84.0	20	US-08-738-652-54	Sequence 54, Appl
43	16.8	84.0	20	US-09-030-701-42	Sequence 42, Appl
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45	16.8	84.0	20	US-09-286-098-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-133-774-12
Sequence 12, Application US/09133774B
Patent No. 5962636
GENERAL INFORMATION:
APPLICANT: Bachmaier, Kurt
APPLICANT: Hessel, Andrew J.
APPLICANT: Neu M.D., Nikolaus
APPLICANT: Penninger, Josef M.
TITLE OF INVENTION: No. 5962636[Peptides Capable of Modulating Inflammatory Heart
FILE REFERENCE: A-536
CURRENT APPLICATION NUMBER: US/09/133, 774B
CURRENT FILING DATE: 1998-08-12
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 12
LENGTH: 20
TYPE: DNA
ORGANISM: Chlamydia trachomatis
FEATURE:
OTHER INFORMATION: An oligonucleotide derived from the DNA encoding a
OTHER INFORMATION: 60 kDa cysteine rich outer membrane protein from
US-09-133-774-12

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cv 1 TCCATGACGTTCTTGACGTT 20
Db 1 TCCATGACGTTCTTGACGTT 20

RESULT 2
US-09-303-862-12
Sequence 12, Application US/09303862
Patent No. 6034230
GENERAL INFORMATION:
APPLICANT: Bachmaier, Kurt
APPLICANT: Hessel, Andrew J.
APPLICANT: Neu M.D., Nikolaus
APPLICANT: Penninger, Josef M.
TITLE OF INVENTION: No. 6034230[Peptides Capable of Modulating Inflammatory Heart
FILE REFERENCE: A-536
CURRENT APPLICATION NUMBER: US/09/303, 862
CURRENT FILING DATE: 1999-05-03
EARLIER APPLICATION NUMBER: 09/133, 774

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GenBank - nucleic search, using sw model

March 31, 2005, 17:02:04 / Search time 1533 Seconds
(Without alignments)
632.162 Million cell updates/sec

US-09-914-454B-1

Sequence: 1 tccatgacgttcctgacgtt 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Sequenced: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

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1: gb_da: *
2: gb_hlg: *
3: gb_in: *
4: gb_cm: *
5: gb_ov: *
6: gb_pal: *
7: gb_pl: *
8: gb_pl: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Alt No.	Score	Query Match	Length	DB	ID	Description
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5	20	100.0	20	6	AR154681	AR154681 Sequence
6	20	100.0	20	6	BD190417	BD190417 Microemul
7	20	100.0	20	6	BD205610	BD205610 Method of
8	20	100.0	20	6	BD205615	BD205615 Method of
9	20	100.0	20	6	BD222610	BD222610 Compositi
10	20	100.0	20	6	BD251265	BD251265 Enhance
11	20	100.0	20	6	BD261152	BD261152 Methods a
12	20	100.0	20	6	BD261157	BD261157 Methods a
13	20	100.0	20	6	BD261307	BD261307 Methods a
14	20	100.0	20	6	BD261311	BD261311 Methods a
15	20	100.0	20	6	BD261560	BD261560 Vaccine
16	20	100.0	20	6	BD267913	BD267913 Methods f
17	20	100.0	20	6	BD270813	BD270813 Stereoi
18	20	100.0	20	6	BD270817	BD270817 Stereoi
19	20	100.0	20	6	CQ753470	CQ753470 Sequence

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22	20	100.0	20	6	CQ774838	CQ774838 Sequence
23	20	100.0	20	6	CQ788113	CQ788113 Sequence
24	20	100.0	20	6	CQ788199	CQ788199 Sequence
25	20	100.0	20	6	CQ815135	CQ815135 Sequence
26	20	100.0	20	6	CQ829537	CQ829537 Sequence
27	20	100.0	20	6	CQ829540	CQ829540 Sequence
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36	20	100.0	20	6	AR316578	AR316578 Sequence
37	20	100.0	20	6	AR432433	AR432433 Sequence
38	20	100.0	20	6	AR528730	AR528730 Sequence
39	20	100.0	20	6	AR532211	AR532211 Sequence
40	20	100.0	20	6	AR534229	AR534229 Sequence
41	20	100.0	20	6	AR535276	AR535276 Sequence
42	20	100.0	20	6	AX015197	AX015197 Sequence
43	20	100.0	20	6	AX020947	AX020947 Sequence
44	20	100.0	20	6	AX020953	AX020953 Sequence
45	20	100.0	20	6	AX040168	AX040168 Sequence

ALIGNMENTS

RESULT 1
LOCUS AR078395 20 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 12 from patent US 5962636.
ACCESSION AR078395
VERSION AR078395.1 GI:10005141
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
AUTHORS Bachmaier K., Hessel A., John., Neu N. and Penninger J Martin.
TITLE Peptides capable of modulating inflammatory heart disease
JOURNAL Patent: US 5962636-A 12-05-OCT-1999;
FEATURES
Location/Qualifiers
1..20
/organism="Unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 TCCATGACGTTCCTGACGTT 20
Db 1 TCCATGACGTTCCTGACGTT 20

RESULT 2

LOCUS AR140451 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 10 from patent US 6207646.
ACCESSION AR140451
VERSION AR140451.1 GI:14482947
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 20)
AUTHORS Kriegl A.M., Kline J., Klinman D. and Steinberg A.D.
TITLE Immunostimulatory nucleic acid molecules

GenCore version 5.1.6
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US-09-914-454b-1

March 31, 2005, 16:54:48 / Search time 255 seconds
(without alignments)
464.293 Million cell updates/sec

US-09-914-454b-1
Perfect score: 20
Sequence: 1 tccatgacctctcctgacct 20
Scoring table: IDENTITY NUC
Gapop 10_0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8760412

Minimum DB seq length: 0
Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: N_Geneseq_16Dec04:*

- 1: Geneseq19808:*
- 2: Geneseq19908:*
- 3: Geneseq20008:*
- 4: Geneseq2001as:*
- 5: Geneseq2001bs:*
- 6: Geneseq2002as:*
- 7: Geneseq2002bs:*
- 8: Geneseq2003as:*
- 9: Geneseq2003bs:*
- 10: Geneseq2003cs:*
- 11: Geneseq2003ds:*
- 12: Geneseq2004as:*
- 13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	AAV60950	AAV60950 umethyly
2	20	100.0	20	AAV47683	AAV47683 umethyly
3	20	100.0	20	AAV27667	AAV27667 Immunost
4	20	100.0	20	AAZ41946	AAZ41946 IL-12 sec
5	20	100.0	20	AAZ41949	AAZ41949 IL-12 sec
6	20	100.0	20	AAV78802	AAV78802 HPV fusio
7	20	100.0	20	AAZ31943	AAZ31943 Cpg adjuv
8	20	100.0	20	AAV74237	AAV74237 Cpg-N mot
9	20	100.0	20	AAV74244	AAV74244 Cpg-N mot
10	20	100.0	20	AAV74242	AAV74242 Cpg-N mot
11	20	100.0	20	AAV8536	AAV8536 Cytosine-
12	20	100.0	20	AAZ28191	AAZ28191 Chlamydia
13	20	100.0	20	AAZ61012	AAZ61012 Nucleotid
14	20	100.0	20	AAZ61010	AAZ61010 Nucleotid
15	20	100.0	20	AAZ48025	AAZ48025 Immune re
16	20	100.0	20	AAZ48022	AAZ48022 Immune re
17	20	100.0	20	AAZ47885	AAZ47885 Immunost
18	20	100.0	20	AAZ47887	AAZ47887 Immunost
19	20	100.0	20	AAZ90447	AAZ90447 Cpg adjuv
20	20	100.0	20	AAZ99174	AAZ99174 Inflammat

21	20	100.0	20	AAZ99004	AAZ99004 Cpg motif
22	20	100.0	20	AAZ47601	AAZ47601 Murine im
23	20	100.0	20	AAZ60277	AAZ60277 Immunost
24	20	100.0	20	AAZ64136	AAZ64136 Immunost
25	20	100.0	20	AAH20390	AAH20390 Cpg motif
26	20	100.0	20	AAH20392	AAH20392 Cpg motif
27	20	100.0	20	AAH50580	AAH50580 Cpg motif
28	20	100.0	20	AAH19260	AAH19260 Cpg motif
29	20	100.0	20	AAZ98805	AAZ98805 Cpg immu
30	20	100.0	20	AAZ59506	AAZ59506 Immunost
31	20	100.0	20	AAZ59501	AAZ59501 Immunost
32	20	100.0	20	AAZ82106	AAZ82106 Oligonuci
33	20	100.0	20	AAZ98748	AAZ98748 Immunost
34	20	100.0	20	AAZ98745	AAZ98745 Immunost
35	20	100.0	20	AAZ98944	AAZ98944 Immunost
36	20	100.0	20	AAZ99175	AAZ99175 Immunost
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44	20	100.0	20	AAZ99175	AAZ99175 Immunost
45	20	100.0	20	AAZ99175	AAZ99175 Immunost

ALIGNMENTS

RESULT 1
ID AAV60950 standard; DNA; 20 BP.
XX AAV60950;
AC
XX
DT 14-DEC-1998 (first entry)
XX
DE Umethylated cytosine-guanine dinucleotide containing oligonucleotide 1.
XX
KW ss; umethylated Cpg dinucleotide; immune response; natural killer cell;
KW Th2 response; Th1 response; Th1 cytokine; hepatitis B.
XX
OS Synthetic.
XX
PN W09840100-A1.
XX
PD 17-SEP-1998.
XX
PF 10-MAR-1998; 98WU-US004703.
XX
PR 10-MAR-1997; 97US-0040376P.
XX
PA (OTTA-) OTTAWA CIVIC LOEB RES INST.
XX (OIA-) OIA GEN GMBH.
XX (IOWA) UNIV IOWA RES FOUND.
XX
PI Davis HL, Schorr J, Krieg AM;
XX WPI; 1998-520792/44.
XX
DR Use of oligonucleotides containing an umethylated Cpg dinucleotide -
XX useful as, e.g. adjuvant with antigen, or nucleic acid encoding antigen
XX for inducing immune response in subject.
XX
PS Claim 14; Page 35; 67pp; English.
XX
CC Oligonucleotides containing at least 1 umethylated Cpg dinucleotide
XX affect the immune response in a subject by activating natural killer
XX cells or redirecting a subject's immune response from a Th1
XX response by inducing monocytic and other cells to produce Th1 cytokines.
XX These nucleic acids containing at least 1 umethylated Cpg can be used as
XX an adjuvant, specifically to induce an immune response against an